

<!--StartFragment-->GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 29, 2008, 14:08:24 ; Search time 532 Seconds
(without alignments)
2415.068 Million cell updates/sec

Title: US-10-532-944-8
Perfect score: 4230
Sequence: 1 MGMIHEQTDFTTSEAIRPDT.....FTPDDVREARAQGISFSIHV 781

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5032670 seqs, 1645091341 residues

Total number of hits satisfying chosen parameters: 5032670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_12.1:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3937	93.1	728	2	Q9RHZ2_ALIAC	Q9rhz2 alicyclobac
2	1937	45.8	787	1	AGL2_BACTQ	Q9f234 bacillus th
3	1888	44.6	779	2	Q2B942_9BACI	Q2b942 bacillus sp
4	1739.5	41.1	801	2	Q2AET1_9FIRM	Q2aet1 halothermot
5	1670	39.5	763	2	Q724N0_LISMF	Q724n0 listeria mo
6	1665.5	39.4	764	2	A4DZ14_LISMO	A4dz14 listeria mo
7	1665	39.4	763	2	Q8YAE7_LISMO	Q8yae7 listeria mo
8	1663	39.3	763	2	A3GEH3_LISMO	A3geh3 listeria mo
9	1663	39.3	763	2	A4DI93_LISMO	A4di93 listeria mo
10	1662.5	39.3	763	2	Q4EI93_LISMO	Q4ei93 listeria mo
11	1659.5	39.2	764	2	A4DAQ6_LISMO	A4daq6 listeria mo
12	1653.5	39.1	763	2	Q92F84_LISIN	Q92f84 listeria in
13	1651.5	39.0	763	2	A3FXQ0_LISMO	A3fxq0 listeria mo
14	1651.5	39.0	763	2	Q4ERP5_LISMO	Q4erp5 listeria mo
15	1651.5	39.0	763	2	A4DR94_LISMO	A4dr94 listeria mo
16	1651.5	39.0	763	2	A3FYZ7_LISMO	A3fyz7 listeria mo
17	1531	36.2	803	2	Q1AU85_RUBXD	Q1au85 rubrobacter
18	1506	35.6	281	2	Q9WX33_ALIAC	Q9wx33 alicyclobac
19	1475	34.9	808	2	A0NI45_OENOE	A0ni45 oenococcus
20	1457	34.4	790	2	A6LTE1_CLOBE	A6lte1 clostridium

21	1453.5	34.4	752	2	Q0ERR0_THEET	Q0err0 thermoanaer
22	1453	34.3	782	2	A4BEH4_9GAMM	A4beh4 reinekea sp
23	1452	34.3	811	2	Q2JSE3_SYNJA	Q2jse3 synechococc
24	1451.5	34.3	752	2	Q3CJW2_THEET	Q3cjw2 thermoanaer
25	1451	34.3	751	2	Q8RDL1_THETN	Q8rdl1 thermoanaer
26	1436.5	34.0	820	2	Q2JLQ6_SYNJB	Q2jql6 synechococc
27	1430.5	33.8	752	2	A6NAA1_THEET	A6naa1 thermoanaer
28	1402	33.1	828	2	Q1ITZ5_ACIBL	Q1itz5 acidobacter
29	1398.5	33.1	779	2	Q8YN00_ANASP	Q8yn00 anabaena sp
30	1397	33.0	756	2	Q0LC91_HERAU	Q0lc91 herpetosiph
31	1396.5	33.0	799	2	Q099U6_STIAU	Q099u6 stigmatella
32	1381.5	32.7	768	2	Q74HN8_LACJO	Q74hn8 lactobacill
33	1371.5	32.4	776	2	Q7NP60_GLOVI	Q7np60 gloeobacter
34	1368.5	32.4	767	2	Q5FI60_LACAC	Q5fi60 lactobacill
35	1358	32.1	792	2	Q040V5_LACGA	Q040v5 lactobacill
36	1349	31.9	768	2	Q1UA36_LACRE	Q1ua36 lactobacill
37	1348	31.9	768	2	A5VKA3_LACRE	A5vka3 lactobacill
38	1344	31.8	768	2	Q0GL90_LACRE	Q0gl90 lactobacill
39	1341.5	31.7	814	2	Q3DX78_CHLAU	Q3dx78 chloroflexu
40	1339	31.7	825	2	A0H583_9CHLR	A0h583 chloroflexu
41	1337.5	31.6	766	2	Q88SA1_LACPL	Q88sa1 lactobacill
42	1335.5	31.6	823	2	A6E786_9SPHI	A6e786 pedobacter
43	1328.5	31.4	798	2	Q091G4_STIAU	Q091g4 stigmatella
44	1313.5	31.1	845	2	Q2B3F7_9BACI	Q2b3f7 bacillus sp
45	1299	30.7	746	2	Q8XIN9_CLOPE	Q8xin9 clostridium

ALIGNMENTS

RESULT 1

Q9RHZ2_ALIAC

ID Q9RHZ2_ALIAC Unreviewed; 728 AA.

AC Q9RHZ2;

DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.

DT 01-MAY-2000, sequence version 1.

DT 24-JUL-2007, entry version 22.

DE Putative alpha-glucosidase.

GN Name=glcA;

OS Alicyclobacillus acidocaldarius (Bacillus acidocaldarius).

OC Bacteria; Firmicutes; Bacillales; Alicyclobacillaceae;

OC Alicyclobacillus.

OX NCBI_TaxID=1388;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 27009;

RX MEDLINE=20507797; PubMed=11053372;

RX DOI=10.1128/JB.182.22.6292-6301.2000;

RA Hulsman A., Lurz R., Scheffel F., Schneider E.;

RT "Maltose and maltodextrin transport in the thermoacidophilic gram-

RT positive bacterium Alicyclobacillus acidocaldarius is mediated by a

RT high-affinity transport system that includes a maltose binding protein

RT tolerant to low pH.";

RL J. Bacteriol. 182:6292-6301(2000).

CC

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DR EMBL: AJ252161; CAB5656.1; -; Genomic_DNA.

DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA:InterPro.

DR GO: GO:0005975; P:carbohydrate metabolic process; IEA:InterPro.

DR InterPro; IPR000322; Glyco_hydro_31.
 DR PANTHER; PTHR22762; Glyco_hydro_31; 1.
 DR Pfam; PF01055; Glyco_hydro_31; 1.
 DR PROSITE; PS00129; GLYCOSYL_HYDROL_F31_1; 1.
 PE 4: Predicted;
 SQ SEQUENCE 728 AA; 82972 MW; 49FC605F929409A0 CRC64;

Query Match 93.1%; Score 3937; DB 2; Length 728;
 Best Local Similarity 100.0%; Pred. No. 3.2e-289;
 Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	54	MVGVAALDDTVLRVAYCRSPGEMPTSTPAIVEQMSQRHSWRLVQEERRVQLECVAGWQIQ	113
Db	1	MVGVAALDDTVLRVAYCRSPGEMPTSTPAIVEQMSQRHSWRLVQEERRVQLECVAGWQIQ	60
Qy	114	INRDDGTWSIRHLGFGTAVEAITWYKRKKGALTFASLDNARFYGLGEKPGPLDKRHEAY	173
Db	61	INRDDGTWSIRHLGFGTAVEAITWYKRKKGALTFASLDNARFYGLGEKPGPLDKRHEAY	120
Qy	174	TMWNSDVYAPHVPEMEALYLSIPFFLRLQDQTA VGIFVDNPGRSRDFRSRYPDVEISTE	233
Db	121	TMWNSDVYAPHVPEMEALYLSIPFFLRLQDQTA VGIFVDNPGRSRDFRSRYPDVEISTE	180
Qy	234	RGLDVGVIIFGASLKDVIIRRYTKLTGRMPMPKWKALGYHQSRYSETQSEVLSVAQTIVE	293
Db	181	RGLDVGVIIFGASLKDVIIRRYTKLTGRMPMPKWKALGYHQSRYSETQSEVLSVAQTIVE	240
Qy	294	RDIPVDALYLDIHYMDGYRVFTFDERRFDPARMCDLRLKLGVRVVPIDVPGVKQDPEYP	353
Db	241	RDIPVDALYLDIHYMDGYRVFTFDERRFDPARMCDLRLKLGVRVVPIDVPGVKQDPEYP	300
Qy	354	VYMDGLAHNHFCQTAEGQVYLGEVWPGLSAFPDFASEEVRWVGKWHRYVTQMIGIEIWN	413
Db	301	VYMDGLAHNHFCQTAEGQVYLGEVWPGLSAFPDFASEEVRWVGKWHRYVTQMIGIEIWN	360
Qy	414	DMNEPAVFNETKTMDDVNVVHRGDGRLYTHGEVHNLYGFWMAEATYRGLKAQLAGKRPFVL	473
Db	361	DMNEPAVFNETKTMDDVNVVHRGDGRLYTHGEVHNLYGFWMAEATYRGLKAQLAGKRPFVL	420
Qy	474	TRAGYSGIQRVAAVWTGDNRSFWEHMMAAIPMVLNMGMSGIPLGGPDVGGFAHSHASGELL	533
Db	421	TRAGYSGIQRVAAVWTGDNRSFWEHMMAAIPMVLNMGMSGIPLGGPDVGGFAHSHASGELL	480
Qy	534	ARWTQMGAFPPFFRNHSAMGTHRQEPWAFGPTFEAVIRRAIRLRYRFLPYLYTLAREAHE	593
Db	481	ARWTQMGAFPPFFRNHSAMGTHRQEPWAFGPTFEAVIRRAIRLRYRFLPYLYTLAREAHE	540
Qy	594	TGLPMRPLVLEYPDDPNTHVDDQFLVGSDDLVPILKPGMAHRMVYLPDGEWIDYETR	653
Db	541	TGLPMRPLVLEYPDDPNTHVDDQFLVGSDDLVPILKPGMAHRMVYLPDGEWIDYETR	600
Qy	654	ERYQGRQYILTYAPLDRIPLYVRAGSAIPVNLERSGETQLGWEIFVDANGRASGRCYED	713
Db	601	ERYQGRQYILTYAPLDRIPLYVRAGSAIPVNLERSGETQLGWEIFVDANGRASGRCYED	660
Qy	714	DGETFSYEDGAYCDRLVALATSEGTLECHLVQSGDGGSLVSVRVFTPDVREARAQ	773
Db	661	DGETFSYEDGAYCDRLVALATSEGTLECHLVQSGDGGSLVSVRVFTPDVREARAQ	720
Qy	774	GISFSIHV 781	

Db 721 GISFSIHV 728

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